Suppose you have a file named "data.txt" containing important information. Display the first 10 lines of this file to quickly glance at its contents using a command.

* nano data.txt
* head -10 data.txt

Now, to check the end of the file for any recent additions, display the last 5 lines of "data.txt" using another command.

* tail -5 data.txt

In a file named "numbers.txt," there are a series of numbers. Display the first 15 lines of this file to analyze the initial data set.

* nano numbers.txt
* head -15 numbers.txt

To focus on the last few numbers of the dataset, display the last 3 lines of "numbers.txt".

* tail -3 numbers.txt

Imagine you have a file named "input.txt" with text content. Use a command to translate all lowercase letters to uppercase in "input.txt" and save the modified text in a new file named "output.txt."

* dd if=input.txt of=output.txt conv=ucase

In a file named "duplicate.txt," there are several lines of text, some of which are duplicates. Use a command to display only the unique lines from "duplicate.txt."

* uniq duplicate.txt

In a file named "fruit.txt," there is a list of fruits, but some fruits are repeated. Use a command to display each unique fruit along with the count of its occurrences in "fruit.txt."

* sort fruit.txt | uniq -c